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## RAW SEQUENCE LISTING

DATE: 05/13/2003

PATENT APPLICATION: US/10/044,569B

TIME: 11:57:39

Input Set : N:\AMC\C1968-US.ST25.txt

Output Set: N:\CRF4\05132003\J044569B.raw

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3 <110> APPLICANT: D. Collen Research Foundation vzw
4     Jacquemin, Marc G
5     Saint-Remy, Jean-Marie R
7 <120> TITLE OF INVENTION: Method and pharmaceutical composition for preventing
8     and/or treating systemic inflammatory response syndrome
10 <130> FILE REFERENCE: C1968
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/044,569B
C--> 12 <141> CURRENT FILING DATE: 2002-01-11
12 <150> PRIOR APPLICATION NUMBER: US 60/261,405
13 <151> PRIOR FILING DATE: 2001-01-11
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 450
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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31 <222> LOCATION: (1)..(450)
32 <223> OTHER INFORMATION:
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36 <222> LOCATION: (130)..(159)
37 <223> OTHER INFORMATION: complementary determining region number one
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40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (202)..(258)
42 <223> OTHER INFORMATION: complementary determining region number two
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (343)..(375)
47 <223> OTHER INFORMATION: complementary determining region number three
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51 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
52 1             5             10             15
54 acc cac gcc cag gtc caa ctg gta cag tct ggg gct gag gtg aag aag      96
55 Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
56             20             25             30

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58 cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc      144
59 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu
60      35      40      45
62 act gaa tta ccc gtg cac tgg gtc gga cag gct cct gga aaa ggg ctt      192
63 Thr Glu Leu Pro Val His Trp Val Gly Gln Ala Pro Gly Lys Gly Leu
64      50      55      60
66 gag tgg gtg gga agt ttt gat cct gaa agt gga gaa tca atc tac gca      240
67 Glu Trp Val Gly Ser Phe Asp Pro Glu Ser Gly Glu Ser Ile Tyr Ala
68 65      70      75      80
70 cgg gag ttc cag ggc agc gtc acc atg acc gcg gac aca tct aca gac      288
71 Arg Glu Phe Gln Gly Ser Val Thr Met Thr Ala Asp Thr Ser Thr Asp
72      85      90      95
74 ata gcc tac atg gag ctg agc agc ctg aga tct gac gac acg gcc gtg      336
75 Ile Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
76      100      105      110
78 tat tac tgt gca gtc cct gac cct gat gct ttt gat atc tgg ggc caa      384
79 Tyr Tyr Cys Ala Val Pro Asp Pro Asp Ala Phe Asp Ile Trp Gly Gln
80      115      120      125
82 ggg aca atg gtc acc gtc tct tca gcc tcc acc aag ggc cca tcg gtc      432
83 Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
84      130      135      140
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87 Phe Pro Leu Gly Ser Arg
88 145      150
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98 <222> LOCATION: (130)..(159)
99 <223> OTHER INFORMATION: complementary determining region number one
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102 <221> NAME/KEY: misc_feature
103 <222> LOCATION: (202)..(258)
104 <223> OTHER INFORMATION: complementary determining region number two
106 <220> FEATURE:
107 <221> NAME/KEY: misc_feature
108 <222> LOCATION: (343)..(375)
109 <223> OTHER INFORMATION: complementary determining region number three
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117 Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
118      20      25      30
121 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu
122      35      40      45
125 Thr Glu Leu Pro Val His Trp Val Gly Gln Ala Pro Gly Lys Gly Leu
126      50      55      60

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129 Glu Trp Val Gly Ser Phe Asp Pro Glu Ser Gly Glu Ser Ile Tyr Ala
130 65              70              75              80
133 Arg Glu Phe Gln Gly Ser Val Thr Met Thr Ala Asp Thr Ser Thr Asp
134              85              90              95
137 Ile Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
138              100             105             110
141 Tyr Tyr Cys Ala Val Pro Asp Pro Asp Ala Phe Asp Ile Trp Gly Gln
142              115             120             125
145 Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
146              130             135             140
149 Phe Pro Leu Gly Ser Arg
150 145              150

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153 &lt;210&gt; SEQ ID NO: 3

154 &lt;211&gt; LENGTH: 426

155 &lt;212&gt; TYPE: DNA

156 &lt;213&gt; ORGANISM: Homo sapiens

158 &lt;220&gt; FEATURE:

159 &lt;221&gt; NAME/KEY: V\_region

160 &lt;222&gt; LOCATION: (1)..(426)

161 &lt;223&gt; OTHER INFORMATION:

163 &lt;220&gt; FEATURE:

164 &lt;221&gt; NAME/KEY: CDS

165 &lt;222&gt; LOCATION: (1)..(426)

166 &lt;223&gt; OTHER INFORMATION:

W--&gt; 168 &lt;220&gt;

169 &lt;221&gt; NAME/KEY: misc\_feature

170 &lt;222&gt; LOCATION: (127)..(162)

171 &lt;223&gt; OTHER INFORMATION: complementary determining region number one

W--&gt; 173 &lt;220&gt;

174 &lt;221&gt; NAME/KEY: misc\_feature

175 &lt;222&gt; LOCATION: (205)..(225)

176 &lt;223&gt; OTHER INFORMATION: complementary determining region number two

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179 &lt;221&gt; NAME/KEY: misc\_feature

180 &lt;222&gt; LOCATION: (325)..(351)

181 &lt;223&gt; OTHER INFORMATION: complementary determining region number three

183 &lt;400&gt; SEQUENCE: 3

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185 Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro

186 1 5 10 15

188 gat acc acc gga gaa att gcg ttg acg cag tct cca ggc acc ctg tct 96

189 Asp Thr Thr Gly Glu Ile Ala Leu Thr Gln Ser Pro Gly Thr Leu Ser

190 20 25 30

192 ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144

193 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser

194 35 40 45

196 ttt agc agc agc tac tta gcc tgg tat cag cag aaa cct ggc cag gct 192

197 Phe Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala

198 50 55 60

## RAW SEQUENCE LISTING

DATE: 05/13/2003

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TIME: 11:57:39

Input Set : N:\AMC\C1968-US.ST25.txt

Output Set: N:\CRF4\05132003\J044569B.raw

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200 ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act ggc atc cca      240
201 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
202 65              70              75              80
204 gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc      288
205 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
206              85              90              95
208 agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag aag tat      336
209 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Lys Tyr
210              100              105              110
212 ggt acg tca gcg atc acc ttc ggg caa ggg aca cga ctg gag att aaa      384
213 Gly Thr Ser Ala Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
214              115              120              125
216 gga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct      426
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218              130              135              140
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222 <211> LENGTH: 142
223 <212> TYPE: PRT
224 <213> ORGANISM: Homo sapiens
226 <220> FEATURE:
227 <221> NAME/KEY: misc_feature
228 <222> LOCATION: (127)..(162)
229 <223> OTHER INFORMATION: complementary determining region number one
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (205)..(225)
234 <223> OTHER INFORMATION: complementary determining region number two
236 <220> FEATURE:
237 <221> NAME/KEY: misc_feature
238 <222> LOCATION: (325)..(351)
239 <223> OTHER INFORMATION: complementary determining region number three
241 <400> SEQUENCE: 4
243 Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
244 1              5              10              15
247 Asp Thr Thr Gly Glu Ile Ala Leu Thr Gln Ser Pro Gly Thr Leu Ser
248              20              25              30
251 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
252              35              40              45
255 Phe Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
256              50              55              60
259 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
260 65              70              75              80
263 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
264              85              90              95
267 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Lys Tyr
268              100              105              110
271 Gly Thr Ser Ala Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
272              115              120              125
275 Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser

```

## RAW SEQUENCE LISTING

DATE: 05/13/2003

PATENT APPLICATION: US/10/044,569B

TIME: 11:57:39

Input Set : N:\AMC\C1968-US.ST25.txt

Output Set: N:\CRF4\05132003\J044569B.raw

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280 <211> LENGTH: 468
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286 <222> LOCATION: (1)..(468)
287 <223> OTHER INFORMATION:
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291 <222> LOCATION: (1)..(468)
292 <223> OTHER INFORMATION:
W--> 294 <220>
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296 <222> LOCATION: (124)..(192)
297 <223> OTHER INFORMATION: complementary determining region number one
W--> 299 <220>
300 <221> NAME/KEY: misc_feature
301 <222> LOCATION: (232)..(285)
302 <223> OTHER INFORMATION: complementary determining region number two
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305 <221> NAME/KEY: misc_feature
306 <222> LOCATION: (282)..(435)
307 <223> OTHER INFORMATION: complementary determining region number three
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311 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Thr Gly
312 1      5      10      15
314 gcc cac tcc cag gtg caa ctg gtg caa tct ggg gct gag gtg aag aag      96
315 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
316      20      25      30
318 cct ggg gcc tca gtg aag gtc tcc tgc aag acc tct gga tac aac ttc      144
319 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
320      35      40      45
322 acc ggc tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac      192
323 Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
324      50      55      60
326 tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc      240
327 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
328 65      70      75      80
330 aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg      288
331 Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
332      85      90      95
334 gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg      336
335 Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
336      100      105      110
338 agc agg ctg aca tct gac gac acg gcc atg tat tac tgt gcg aga gcc      384
339 Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala

```

## VERIFICATION SUMMARY

DATE: 05/13/2003

PATENT APPLICATION: US/10/044,569B

TIME: 11:57:40

Input Set : N:\AMC\C1968-US.ST25.txt

Output Set: N:\CRF4\05132003\J044569B.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
L:39 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:32  
L:168 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:161  
L:173 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:166  
L:294 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:287  
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:292  
L:428 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:421  
L:433 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:426